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(54) Title: **HUMAN GENES AND GENE EXPRESSION PRODUCTS**

(57) Abstract: This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, e.g., these genes and proteins, including probes, antisense constructs, and antibodies.

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Table 3A Nearest Neighbor (BlastN vs. Genbank)			
SEQ ID NO	ACCESSION	DESCRIP	P VALUE
1395	AF378868	Arabidopsis thaliana AT5g11200/F2I11_90 mRNA, complete cds	2.5
1396	AF328539	Homo sapiens clone 12qtel_c64t3 sequence	0.0003
1397	AE006450	Lactococcus lactis subsp. lactis IL1403 section 212 of 218 of the complete genome	0.47
1398	Z12840	O.cuniculus mRNA for protein of unknown function	2E-97
1399	U31165	Rattus norvegicus SH3 domain binding protein (CR16) gene, exon 6	1.9
1400	Y15005	Bison bonasus mitochondrial cytB gene	1.8
1401	AC091267	Caenorhabditis elegans cosmid Y37B11A, complete sequence	3.7
1402	AB055364	Macaca fascicularis brain cDNA, clone:Qf1A-12522	e-119
1403	NC_001610	Didelphis virginiana mitochondrion, complete genome	0.006
1404	AF362372	Dictyostelium discoideum histidine kinase DhkJ (dhkJ) gene, complete cds	0.055
1405	AF027164	Homo sapiens type II integral membrane protein (NKG2-E) gene, partial cds; and type II integral membrane protein (NKG2-F) gene, complete cds	3.6
1406	M76376	Human cysteine-rich protein (CRP) gene, exon 2	0.027
1407	D31863	Mouse Pig-a gene for GPI-anchor biosynthesis (PIG-A protein), exon 6 and complete cds	0.026
1408	XM_031315	Homo sapiens hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit (FLJ14033), mRNA	0.000007
1409	AY019369	Oryza sativa microsatellite MRG1694 containing (AT)X32, genomic sequence	0.0001
1410	AF067610	Caenorhabditis elegans cosmid F41A4	0.084
1411	AJ401391	Drosophila melanogaster mRNA for PDGF/VEGF-like protein (CG7103 gene)	0.18
1412	XM_008417	Homo sapiens hypothetical protein FLJ20694 (FLJ20694), mRNA	0.0000001
1413	AF242195	Homo sapiens KLK15 (KLK15) gene, complete cds, alternatively spliced	e-160
1414	Y14077	Bacillus subtilis 10.6 Kb chromosomal DNA: glyB-prsA region	0.008
1415	AE006802	Sulfolobus solfataricus section 161 of 272 of the complete genome	0.057
1416	AY007149	Homo sapiens clone CDABP0086 mRNA sequence	0.092
1417	K02628	Oxytricha nova (hypotrichous ciliate) (clones LMiC2-(5,6,8)) micronuclear DNA, C2 gene (version 3), complete cds	0.063
1419	X14260	Xenopus tropicalis alpha-globin gene	1.7
1420	AJ401391	Drosophila melanogaster mRNA for PDGF/VEGF-like protein (CG7103 gene)	0.15
1421	XM_032580	Homo sapiens nebullette (NEBL), mRNA	1.3
1422	XM_008060	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 (SLC7A5), mRNA	2E-12
1424	AF035820	Hordeum vulgare gibberellin action negative regulator SPY mRNA, complete cds	2.1

Table 3A Nearest Neighbor (BlastN vs. Genbank)			
SEQ ID NO	ACCESSN	DESCRIP	P VALUE
5297	XM_032347	Homo sapiens region containing TLS-associated serine-arginine protein 1; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 2; TLS-associated serine-arginine protein 1; TLS-associa>	0
5298	Z63116	H.sapiens CpG island DNA genomic MseI fragment, clone 78e4, reverse read cpg78e4.rt1a	0.24
5299	AE006833	Sulfolobus solfataricus section 192 of 272 of the complete genome	6.4
5300	XM_032811	Homo sapiens similar to ZINC FINGER PROTEIN 20 (ZINC FINGER PROTEIN KOX13) (DKFZP572P0920) (H. sapiens) (LOC90591), mRNA	0.21
5301	AF202552	Homo sapiens DNA methyltransferase (DNMT1) gene, exons 2, 3, and 4	0.23
5302	U92963	Pygathrix roxellana NADH dehydrogenase subunit 3 (ND3) gene, partial cds, tRNA-Arg gene, complete sequence, NADH dehydrogenase subunit 4L (ND4L) and NADH dehydrogenase subunit 4 (ND4) genes, complete cds, and tRNA-His, tRNA-Ser and tRNA-Leu genes, comp>	0.17
5303	Z99833	Euglena deses chloroplast psbC gene: complete group III twintron, complete internal matI gene, partial 5' and 3' psbC exons	4.7
5304	AB047962	Macaca fascicularis brain cDNA, clone:QnpA-13041	e-125
5305	AF159913	Euplotes crassus transposon Tec1 clone Tec1-2 orf 2 and orf 3 pseudogenes, complete sequence	0.5
5306	Y15435	Kluyveromyces lactis PDC1 gene, promoter region	0.087
5307	U67506	Methanococcus jannaschii section 48 of 150 of the complete genome	1.4
5308	U73943	Bacillus subtilis phosphofructokinase I (pfkI) gene, partial cds; and pyruvate kinase I gene, complete cds	2.2
5309	U72027	Bos taurus photoreceptor disk rim specific protein rom-1 (ROM1) mRNA, partial cds	0.06
5310	X16509	Rice alpha-amylase gene	2.1
5312	AB049900	Macaca fascicularis brain cDNA, clone:QnpA-19713	0.01
5313	Z24756	S.pombe rhp51 and rpa1 genes, complete CDS's	0.003
5314	XM_002989	Homo sapiens similar to hypothetical protein FLJ10546 (H. sapiens) (LOC93548), mRNA	5E-62
5316	AL358272	S.pombe chromosome I cosmid c458	0.61
5317	XM_044123	Homo sapiens cadherin 20, type 2 (CDH20), mRNA	4E-48
5318	AF038866	Bacteroides fragilis transposon Tn5520 transposase (bipH) and mobilization protein BmpH (bmpH) genes, complete cds	0.73
5319	AF332577	Homo sapiens prosomal P27K protein (PSMA6) gene, partial cds	2E-51
5320	X68650	O.cuniculus mRNA for ryanodine receptor	0.55
5321	XM_038450	Homo sapiens hypothetical protein FLJ20694 (FLJ20694), mRNA	0

Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1402	478809	gi 478809 pir S29851 protein kinase 6 (EC 2.7.1.-) - soybean gb AAA34002.1  (M67449) protein kinase [Glycine max] prf 1908223A protein kinase [Glycine max]	9.3
1406	1517936	gi 1517936 gb AAB07000.1  (U52347) tachykinin-like receptor [Stomoxys calcitrans]	1.1
1407	9977929	gi 9977929 sp Q05013 LIPA_NEIMB CAPSULE POLYSACCHARIDE MODIFICATION PROTEIN LIPA pir D81240 capsule polysaccharide modification protein LipA NMB0082 [imported] - Neisseria meningitidis (group B strain MD58) gb AAF40546.1  (AE002367) capsule polysaccharide modification protein LipA [Neisseria meningitidis MC58]	9.3
1412	14773348	gi 14773348 ref XP_038450.1  20849 [Homo sapiens]	1E-48
1413	13537363	gi 13537363 dbj BAB40663.1  (AB051851) death receptor 3 [Homo sapiens]	3.9
1419	7477083	gi 7477083 pir A70577 hypothetical protein Rv2133c - Mycobacterium tuberculosis (strain H37RV) emb CAB08660.1  (Z95388) hypothetical protein Rv2133c [Mycobacterium tuberculosis] gb AAK46475.1  (AE007067) conserved hypothetical protein [Mycobacterium tuberculosis CDC1551]	1.9
1422	7499021	gi 7499021 pir T20846 hypothetical protein F13E9.9 - Caenorhabditis elegans emb CAA93411.1  (Z69383) F13E9.9 [Caenorhabditis elegans]	4.1
1424	14723696	gi 14723696 ref XP_035744.1  hypothetical protein XP_035744 [Homo sapiens]	1.5
1425	9961349	gi 9961349 ref NP_005500.2  Dmx-like 1 [Homo sapiens]	0.94
1426	478302	gi 478302 pir JN0835 carbonate dehydratase (EC 4.2.1.1) I - chimpanzee	1.6
1427	6649942	gi 6649942 gb AAF21641.1 AF032379_1 (AF032379) gonadotrophin releasing hormone receptor; GnRH-R [Trichosurus vulpecula]	9.6
1432	6636500	gi 6636500 gb AAF20201.1 AF205791_1 (AF205791) squalene synthase [Botryococcus braunii]	1.8
1434	7504070	gi 7504070 pir T22586 hypothetical protein F53F4.14 - Caenorhabditis elegans	0.05

Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
1904	5139521	gi 5139521 emb CAB45562.1  (AJ238798) CTRP protein [Plasmodium berghei] dbj BAA82322.1  (AB027129) adhesive protein-like molecule [Plasmodium berghei] gb AAF73158.1 AF149771_1 (AF149771) ookinete protein [Plasmodium berghei]	8
1905	7489900	gi 7489900 pir T18287 protein-tyrosine kinase (EC 2.7.1.112) - slime mold (Dictyostelium discoideum) gb AAB04999.1  (U64830) protein tyrosine kinase [Dictyostelium discoideum]	5.3
1908	6002776	gi 6002776 gb AAF00134.1 AF149806_1 (AF149806) hypothetical protein [Oryza sativa]	0.15
1913	14773348	gi 14773348 ref XP_038450.1  20849 [Homo sapiens]	2E-50
1916	7301187	gi 7301187 gb AAF56319.1  (AE003748) CG5794 gene product [Drosophila melanogaster]	8
1918	3378685	gi 3378685 emb CAA76071.1  (Y16104) replicase protein [Physalis mottle tymovirus]	0.13
1919	4501915	gi 4501915 ref NP_003807.1  a disintegrin and metalloproteinase domain 9 preproprotein; meltrin gamma [Homo sapiens] gb AAC50403.1  (U41766) metalloprotease/disintegrin/cysteine-rich protein precursor [Homo sapiens]	0.002
1922	14587070	gi 14587070 gb AAK70463.1 AF387344_4 (AF387344) spore germination protein GerLC [Bacillus cereus]	8.4
1924	7291161	gi 7291161 gb AAF46595.1  (AE003450) CG2892 gene product [Drosophila melanogaster]	6
1925	7446016	gi 7446016 pir E70895 hypothetical glycine-rich protein Rv1087 - Mycobacterium tuberculosis (strain H37RV) emb CAA17203.1  (AL021897) PE_PGRS [Mycobacterium tuberculosis]	3.6
1926	11595522	gi 11595522 emb CAC18316.1  (AL451022) hypothetical protein [Neurospora crassa]	5.9
1930	14043326	gi 14043326 gb AAH07658.1 AAH07658 (BC007658) Unknown (protein for MGC:747) [Homo sapiens]	8E-76
1931	13810543	gi 13810543 dbj BAB43950.1  (AB051633) ookinete surface protein Pos28-2 [Plasmodium ovale]	3.1
1933	7206826	gi 7206826 gb AAF39985.1  (AC006696) contains similarity to other proline-rich proteins [Caenorhabditis elegans]	6.6

Table 3B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)			
SEQ ID NO	ACCESS N	DESCRIPTION	P VALUE
5304	11467524	gi 11467524 ref NP_043670.1  PSI, subunit III, plastocyanin-binding [Odontella sinensis] sp P49483 PSAF_ODOSI PHOTOSYSTEM I REACTION CENTRE SUBUNIT III (PSI-F) pir S78329 photosystem I chain III - Odontella sinensis chloroplast emb CAA91702.1  (Z67753) PSI, subunit III, plastocyanin-binding [Odontella sinensis]	6.2
5306	7292767	gi 7292767 gb AAF48162.1  (AE003489) CG15927 gene product [Drosophila melanogaster]	6.3
5309	14601766	gi 14601766 ref NP_148307.1  hypothetical protein [Aeropyrum pernix] pir C72501 hypothetical protein APE1985 - Aeropyrum pernix (strain K1) dbj BAA80995.1  (AP000063) 160aa long hypothetical protein [Aeropyrum pernix]	1.8
5310	13661965	gi 13661965 gb AAK38127.1 AC058781_4 (AC058781) L344.4 [Leishmania major]	7.1
5312	6320879	gi 6320879 ref NP_010958.1  Transcriptional activator of nitrogen-regulated genes; Gln3p [Saccharomyces cerevisiae] sp P18494 GLN3_YEAST NITROGEN REGULATORY PROTEIN GLN3 pir S50543 GLN3 protein - yeast (Saccharomyces cerevisiae) gb AAB64575.1  (U18796) Gln3p: Nitrogen regulatory protein [Saccharomyces cerevisiae]	8.5
5313	4493990	gi 4493990 emb CAB39049.1  (AL034559) hypothetical protein, PFC1045c [Plasmodium falciparum]	0.74
5314	10047245	gi 10047245 dbj BAB13411.1  (AB046805) KIAA1585 protein [Homo sapiens]	2E-69
5317	14762995	gi 14762995 ref XP_044123.1  cadherin 20, type 2 [Homo sapiens]	4E-17
5321	14773348	gi 14773348 ref XP_038450.1  20849 [Homo sapiens]	3E-45
5326	4691710	gi 4691710 gb AAD28038.1 AF119712_1 (AF119712) bone morphogenetic protein BMP2/4 [Lytechinus variegatus]	5.4
5328	13161382	gi 13161382 dbj BAB32977.1  (AB034197) lamin B3 [Carassius auratus]	6.9
5333	12654811	gi 12654811 gb AAH01248.1 AAH01248 (BC001248) hypothetical protein FLJ20272 [Homo sapiens]	6.2

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
1180	645900	15,17	9	0	9.66	-1
1180	645900	16,17	9	0	9.14	-1
1180	645900	23,24	7	0	7.07	-1
1185	463824	15,16	6	0	6.34	-1
1185	463824	15,17	6	0	6.44	-1
1185	463824	27,28	0	8	-1	7.39
1185	463824	28,29	8	0	9.97	-1
1193	649617	28,29	5	0	6.23	-1
1208	452738	28,29	5	0	6.23	-1
1234	647232	16,17	9	0	9.14	-1
1234	647232	28,29	6	0	7.48	-1
1237	503122	25,26	8	178	-1	23.05
1237	503122	27,29	12	2	8.09	-1
1237	503122	30,31	22	98	-1	4
1238	515350	15,16	14	0	14.8	-1
1238	515350	15,17	14	3	5.01	-1
1244	648996	15,16	6	0	6.34	-1
1244	648996	15,17	6	0	6.44	-1
1255	416624	27,29	6	0	8.09	-1
1261	449956	12,13	6	0	6.2	-1
1261	449956	16,17	10	1	10.16	-1
1261	449956	28,29	10	0	12.46	-1
1261	449956	30,31	8	1	8.9	-1
1270	380477	15,17	7	0	7.51	-1
1276	645100	15,16	7	0	7.4	-1
1276	645100	15,17	7	0	7.51	-1
1278	554581	28,29	7	0	8.72	-1
1290	650820	16,17	8	0	8.12	-1
1306	646309	16,17	6	0	6.09	-1
1315	502683	15,16	6	0	6.34	-1
1315	502683	28,29	5	0	6.23	-1
1342	463487	15,17	8	1	8.59	-1
1352	446987	15,17	10	0	10.73	-1
1354	640922	27,28	0	7	-1	6.46
1354	640922	28,29	7	0	8.72	-1
1355	561793	30,31	6	0	6.67	-1
1382	649354	15,16	6	0	6.34	-1
1382	649354	15,17	6	0	6.44	-1
1386	507050	27,29	9	0	12.14	-1
1386	507050	28,29	7	0	8.72	-1
1392	649272	16,17	8	0	8.12	-1
1412	453470	15,16	12	1	12.68	-1
1412	453470	15,17	12	1	12.88	-1
1423	419255	15,16	11	0	11.63	-1
1423	419255	15,17	11	1	11.81	-1
1424	648996	15,16	6	0	6.34	-1
1424	648996	15,17	6	0	6.44	-1
1425	451361	23,24	1	8	-1	7.92

SEQ ID NO	CLUSTER	PAIR AB	CLONES A	CLONES B	RATIO PLUS	RATIO MINUS
5281	452142	15,16	1	10	-1	9.46
5281	452142	16,17	10	2	5.08	-1
5282	451994	27,28	4	17	-1	3.92
5297	4244	28,29	8	28	-1	2.81
5308	450262	21,22	0	8	-1	8.13
5308	450262	27,28	30	14	2.32	-1
5308	450262	28,29	14	46	-1	2.64
5311	452506	15,16	8	1	8.46	-1
5311	452506	28,29	6	0	7.48	-1
5313	7022	25,26	7	0	6.76	-1
5313	7022	27,28	4	16	-1	3.69
5313	7022	28,29	16	5	3.99	-1
5315	2930	01,02	3	14	-1	5.06
5315	2930	27,29	5	0	6.75	-1
5315	2930	28,29	7	0	8.72	-1
5317	454226	28,29	5	0	6.23	-1
5321	453470	15,16	12	1	12.68	-1
5321	453470	15,17	12	1	12.88	-1
5324	454050	27,28	0	7	-1	6.46
5338	454518	27,29	6	0	8.09	-1
5338	454518	28,29	6	0	7.48	-1
5350	23649	27,28	37	12	3.34	-1
5350	23649	27,29	37	0	49.92	-1
5350	23649	28,29	12	0	14.95	-1
5357	519109	23,24	1	34	-1	33.65
5360	453783	27,28	0	8	-1	7.39
5360	453783	28,29	8	0	9.97	-1
5365	454509	25,26	7	0	6.76	-1
5365	454509	27,28	6	0	6.5	-1
5366	454562	23,24	13	4	3.28	-1
5366	454562	25,26	7	0	6.76	-1
5370	453783	27,28	0	8	-1	7.39
5370	453783	28,29	8	0	9.97	-1
5373	801	30,31	25	7	3.97	-1
5374	453494	27,28	7	0	7.58	-1
5374	453494	30,31	6	0	6.67	-1
5375	453202	15,16	6	0	6.34	-1
5375	453202	16,17	0	11	-1	10.83
5381	387530	30,31	2	24	-1	10.79
5382	453846	15,17	0	11	-1	10.25
5391	551995	28,29	7	0	8.72	-1
5397	446531	16,17	0	6	-1	5.91
5401	453508	25,26	27	9	2.9	-1
5401	453508	27,28	9	1	9.75	-1
5413	560868	27,29	6	0	8.09	-1
5448	554742	16,17	0	6	-1	5.91
5467	551617	15,16	9	0	9.51	-1
5467	551617	16,17	0	7	-1	6.89



Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1170	40637	0.0	71.4	7.0
1181	42035	0.0	42.9	7.0
1186	43931	0.0	37.5	8.0
1189	46029	0.0	37.5	8.0
1193	42523	0.0	37.5	8.0
1199	39829	0.0	42.9	7.0
1203	43923	0.0	62.5	8.0
1206	43229	0.0	50.0	8.0
1208	44629	0.0	37.5	8.0
1220	43219	0.0	50.0	8.0
1222	39835	0.0	100.0	7.0
1231	40529	0.0	100.0	7.0
1234	43921	0.0	37.5	8.0
1238	45319	0.0	50.0	8.0
1241	45313	0.0	37.5	8.0
1245	44627	0.0	37.5	8.0
1246	44631	0.0	37.5	8.0
1250	40531	0.0	42.9	7.0
1255	46035	0.0	62.5	8.0
1270	41233	0.0	85.7	7.0
1274	40537	0.0	42.9	7.0
1280	44637	0.0	37.5	8.0
1281	45335	0.0	37.5	8.0
1290	40535	0.0	57.1	7.0
1292	41241	0.0	42.9	7.0
1293	41943	0.0	42.9	7.0
1311	41947	0.0	42.9	7.0
1382	38765	0.0	57.1	7.0
1392	39467	0.0	57.1	7.0
1398	42861	0.0	62.5	8.0
1399	43559	0.0	37.5	8.0
1401	38146	0.0	37.5	8.0
1402	43553	0.0	37.5	8.0
1408	43555	0.0	42.9	7.0
1412	39463	0.0	71.4	7.0
1413	43557	0.0	42.9	7.0
1415	40175	0.0	42.9	7.0
1418	40167	0.0	42.9	7.0
1422	40260	0.0	37.5	8.0
1429	44965	0.0	37.5	8.0
1430	44969	0.0	42.9	7.0
1432	44967	0.0	42.9	7.0
1442	40165	0.0	42.9	7.0

Table 8

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
1834	41230	0.0	57.1	7.0
1836	39204	0.0	42.9	7.0
1845	38504	0.0	42.9	7.0
1850	40612	0.0	42.9	7.0
1851	40616	0.0	42.9	7.0
1854	40614	0.0	42.9	7.0
1855	40624	0.0	42.9	7.0
1859	39912	0.0	42.9	7.0
1861	39918	0.0	42.9	7.0
1868	39906	0.0	42.9	7.0
1870	38528	0.0	42.9	7.0
1875	39226	0.0	42.9	7.0
1885	38514	0.0	42.9	7.0
1888	38522	0.0	42.9	7.0
1891	39230	0.0	42.9	7.0
1892	39922	0.0	42.9	7.0
1898	39924	0.0	42.9	7.0
1906	39936	0.0	42.9	7.0
1907	40626	0.0	42.9	7.0
1913	41240	0.0	57.1	7.0
1916	40225	0.0	42.9	7.0
1922	41641	0.0	42.9	7.0
1927	42036	0.0	42.9	7.0
1929	41938	0.0	42.9	7.0
1932	40235	0.0	42.9	7.0
1935	38117	0.0	42.9	7.0
1944	40929	0.0	42.9	7.0
1946	41952	0.0	42.9	7.0
1949	39527	0.0	57.1	7.0
1950	39533	0.0	42.9	7.0
1954	41944	0.0	42.9	7.0
1957	42046	0.0	42.9	7.0
1963	41342	0.0	42.9	7.0
1964	39535	0.0	42.9	7.0
1969	40544	0.0	42.9	7.0
1970	38821	0.0	42.9	7.0
1971	40231	0.0	42.9	7.0
1972	41647	0.0	42.9	7.0
1973	41344	0.0	42.9	7.0
1977	38823	0.0	42.9	7.0
1980	40943	0.0	42.9	7.0
1988	38831	0.0	42.9	7.0
1990	38127	0.0	42.9	7.0

We Claim:

1. An isolated polynucleotide comprising a nucleotide sequence which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOS: 1-6010.

2. An isolated polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence having at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NOS:1-6010, a degenerate variant of SEQ ID NOS:1-6010, an antisense of SEQ ID NOS:1-6010, and a complement of SEQ ID NOS:1-6010.

3. An isolated polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence selected from the group consisting of: SEQ ID NOS:1-6010, a degenerate variant of SEQ ID NOS:1-6010, an antisense of SEQ ID NOS:1-6010, and a complement of SEQ ID NOS:1-6010.

4. The isolated polynucleotide of claim 3, wherein the polynucleotide comprises at least 100 contiguous nucleotides of the nucleotide sequence.

5. The isolated polynucleotide of claim 3, wherein the polynucleotide comprises at least 200 contiguous nucleotides of the selected nucleotide sequence.

6. An isolated polynucleotide comprising a nucleotide sequence of at least 90% sequence identity to a sequence selected from the group consisting of: SEQ ID NOS:1-6010, a degenerate variant of SEQ ID NOS:1-6010, an antisense of SEQ ID NOS:1-6010, and a complement of SEQ ID NOS:1-6010.

7. The isolated polynucleotide of claim 6, wherein the polynucleotide comprises a nucleotide sequence of at least 95% sequence identity to the selected nucleotide sequence.

8. The isolated polynucleotide of claim 6, wherein the polynucleotide comprises a nucleotide sequence that is identical to the selected nucleotide sequence.

9. A polynucleotide comprising a nucleotide sequence of an insert contained in a clone deposited as ATCC Accession No. PTA-2027, PTA-2028, PTA-2029, PTA-2030, PTA-2031, PTA-2032, PTA-2033, PTA-2034, PTA-2035, PTA-2036, PTA-2037, PTA-2038, PTA-2039, PTA-2040, PTA-2041, PTA-2042, PTA-2043, PTA-2044, PTA-2045, PTA-2046, PTA-2047, PTA-2050, PTA-2051, PTA-2052, PTA-2053, PTA-2054, PTA-2055, PTA-2056, PTA-2057, PTA-2058, PTA-

2059, PTA-2060, PTA-2061, PTA-2062, PTA-2048, PTA-2049, PTA-2063, PTA-2064, PTA-2065, PTA-2066, PTA-2067, or PTA-2068.

- 5        10. An isolated cDNA obtained by the process of amplification using a polynucleotide comprising at least 15 contiguous nucleotides of a nucleotide sequence of a sequence selected from the group consisting of SEQ ID NOS:1-6010.

- 10       11. The isolated cDNA of claim 10, wherein the polynucleotide comprises at least 25 contiguous nucleotides of the selected nucleotide sequence.

- 12. The isolated cDNA of claim 10, wherein the polynucleotide comprises at least 100 contiguous nucleotides of the selected nucleotide sequence.

- 15       13. The isolated cDNA of claims 10, 11, or 12, wherein amplification is by polymerase chain reaction (PCR) amplification.

14. An isolated recombinant host cell containing the polynucleotide according to claims 1, 2, 3, 6, 9, or 10.

- 20       15. An isolated vector comprising the polynucleotide according to claims claims 1, 2, 3, 6, 9, or 10.

16. A method for producing a polypeptide, the method comprising the steps of:  
      culturing a recombinant host cell containing the polynucleotide according to claims claims  
25    1, 2, 3, 6, 9, or 10., said culturing being under conditions suitable for the expression of an encoded polypeptide;  
      recovering the polypeptide from the host cell culture.

- 30       17. An isolated polypeptide encoded by the polynucleotide according to claims claims 1, 2, 3, 6, 9, or 10.

18. An antibody that specifically binds the polypeptide of claim 17.

19. A method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene comprising an  
5 identifying sequence of at least one of SEQ ID NOS:1-6010;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

20. A library of polynucleotides, wherein at least one of the polynucleotides comprises the  
10 sequence information of the polynucleotide according to claims 1, 2, 3, 6, 9, or 10.

21. The library of claim 20, wherein the library is provided on a nucleic acid array.

22. The library of claim 20, wherein the library is provided in a computer-readable format.  
15

23. A method of inhibiting tumor growth by modulating expression of a gene product, the gene product being encoded by a gene identified by a sequence selected from the group consisting of SEQ ID NOS:1-6010.

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